

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: St. Geme III, Joseph W.
Falkow, Stanley

(ii) TITLE OF INVENTION: Haemophilus Adherence and Penetration
Protein

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
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(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: United States
(F) ZIP: 94111-4187

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/296,791
(B) FILING DATE: 25-AUG-1994
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Trecartin, Richard F.
(B) REGISTRATION NUMBER: 31,801
(C) REFERENCE/DOCKET NUMBER: A-59941/RFT/RMS

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: both

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 60..4241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCAATAGTCG TTTAACTAGT ATTTTTAAT ACGAAAAATT ACTTAATTAA ATAAACATT 59

ATG AAA AAA ACT GTA TTT CGT CTT AAT TTT TTA ACC GCT TGC ATT TCA 107
Met Lys Lys Thr Val Phe Arg Leu Asn Phe Leu Thr Ala Cys Ile Ser
1 5 10 15

TTA GGG ATA GTA TCG CAA GCG TGG GCT GGT CAC ACT TAT TTT GGG ATT 155

Leu	Gly	Ile	Val	Ser	Gln	Ala	Trp	Ala	Gly	His	Thr	Tyr	Phe	Gly	Ile	
20										25					30	
GAT TAC CAA TAT TAT CGT GAT TTT GCC GAG AAT AAA GGG AAG TTC ACA															203	
Asp	Tyr	Gln	Tyr	Tyr	Arg	Asp	Phe	Ala	Glu	Asn	Lys	Gly	Lys	Phe	Thr	
35										40					45	
GTT GGG GCT CAA AAT ATT AAG GTT TAT AAC AAA CAA GGG CAA TTA GTT															251	
Val	Gly	Ala	Gln	Asn	Ile	Lys	Val	Tyr	Asn	Lys	Gln	Gly	Gln	Leu	Val	
50							55							60		
GGC ACA TCA ATG ACA AAA GCC CCG ATG ATT GAT TTT TCT GTA GTG TCA															299	
Gly	Thr	Ser	Met	Thr	Lys	Ala	Pro	Met	Ile	Asp	Phe	Ser	Val	Val	Ser	
65							70			75				80		
CGT AAC GGC GTG GCA GCC TTG GTT GAA AAT CAA TAT ATT GTG AGC GTG															347	
Arg	Asn	Gly	Val	Ala	Ala	Leu	Val	Glu	Asn	Gln	Tyr	Ile	Val	Ser	Val	
							85			90				95		
GCA CAT AAC GTA GGA TAT ACA GAT GTT GAT TTT GGT GCA GAG GGA AAC															395	
Ala	His	Asn	Val	Gly	Tyr	Thr	Asp	Val	Asp	Phe	Gly	Ala	Glu	Gly	Asn	
100							105							110		
AAC CCC GAT CAA CAT CGT TTT ACT TAT AAG ATT GTA AAA CGA AAT AAC															443	
Asn	Pro	Asp	Gln	His	Arg	Phe	Thr	Tyr	Lys	Ile	Val	Lys	Arg	Asn	Asn	
115							120			125						
TAC AAA AAA GAT AAT TTA CAT CCT TAT GAG GAC GAT TAC CAT AAT CCA															491	
Tyr	Lys	Lys	Asp	Asn	Leu	His	Pro	Tyr	Glu	Asp	Tyr	His	Asn	Pro		
130							135			140						
CGA TTA CAT AAA TTC GTT ACA GAA GCG GCT CCA ATT GAT ATG ACT TCG															539	
Arg	Leu	His	Lys	Phe	Val	Thr	Glu	Ala	Ala	Pro	Ile	Asp	Met	Thr	Ser	
145							150			155				160		
AAT ATG AAT GGC AGT ACT TAT TCA GAT AGA ACA AAA TAT CCA GAA CGT															587	
Asn	Met	Asn	Gly	Ser	Thr	Tyr	Ser	Asp	Arg	Thr	Lys	Tyr	Pro	Glu	Arg	
							165			170				175		
GTT CGT ATC GGC TCT GGA CGG CAG TTT TGG CGA AAT GAT CAA GAC AAA															635	
Val	Arg	Ile	Gly	Ser	Gly	Arg	Gln	Phe	Trp	Arg	Asn	Asp	Gln	Asp	Lys	
180							185			190						
GGC GAC CAA GTT GCC GGT GCA TAT CAT TAT CTG ACA GCT GGC AAT ACA															683	
Gly	Asp	Gln	Val	Ala	Gly	Ala	Tyr	His	Tyr	Leu	Thr	Ala	Gly	Asn	Thr	
195							200			205						
CAC AAT CAG CGT GGA GCA GGT AAT GGA TAT TCG TAT TTG GGA GGC GAT															731	
His	Asn	Gln	Arg	Gly	Ala	Gly	Asn	Gly	Tyr	Ser	Tyr	Leu	Gly	Gly	Asp	
210							215			220						
GTT CGT AAA GCG GGA TAT GGT CCA TTA CCG ATT GCA GGC TCA AAG															779	
Val	Arg	Lys	Ala	Gly	Glu	Tyr	Gly	Pro	Leu	Pro	Ile	Ala	Gly	Ser	Lys	
225							230			235				240		
GGG GAC AGT GGT TCT CCG ATG TTT ATT TAT GAT GCT GAA AAA CAA AAA															827	
Gly	Asp	Ser	Gly	Ser	Pro	Met	Phe	Ile	Tyr	Asp	Ala	Glu	Lys	Gln	Lys	
							245			250				255		
TGG TTA ATT AAT GGG ATA TTA CGG GAA GGC AAC CCT TTT GAA GGC AAA															875	
Trp	Leu	Ile	Asn	Gly	Ile	Leu	Arg	Glu	Gly	Asn	Pro	Phe	Glu	Gly	Lys	
260							265			270						
GAA AAT GGG TTT CAA TTG GTT CGC AAA TCT TAT TTT GAT GAA ATT TTC															923	
Glu	Asn	Gly	Phe	Gln	Leu	Val	Arg	Lys	Ser	Tyr	Phe	Asp	Glu	Ile	Phe	

275

280

285

GAA AGA GAT TTA CAT ACA TCA CTT TAC ACC CGA GCT GGT AAT GGA GTG 971
 Glu Arg Asp Leu His Thr Ser Leu Tyr Thr Arg Ala Gly Asn Gly Val
 290 295 300

TAC ACA ATT AGT GGA AAT GAT AAT GGT CAG GGG TCT ATA ACT CAG AAA 1019
 Tyr Thr Ile Ser Gly Asn Asn Gly Gln Gly Ser Ile Thr Gln Lys
 305 310 315 320

TCA GGA ATA CCA TCA GAA ATT AAA ATT ACG TTA GCA AAT ATG AGT TTA 1067
 Ser Gly Ile Pro Ser Glu Ile Lys Ile Thr Leu Ala Asn Met Ser Leu
 325 330 335

CCT TTG AAA GAG AAG GAT AAA GTT CAT AAT CCT AGA TAT GAC GGA CCT 1115
 Pro Leu Lys Glu Lys Asp Lys Val His Asn Pro Arg Tyr Asp Gly Pro
 340 345 350

AAT ATT TAT TCT CCA CGT TTA AAC AAT GGA GAA ACG CTA TAT TTT ATG 1163
 Asn Ile Tyr Ser Pro Arg Leu Asn Asn Gly Glu Thr Leu Tyr Phe Met
 355 360 365

GAT CAA AAA CAA GGA TCA TTA ATC TTC GCA TCT GAC ATT AAC CAA GGG 1211
 Asp Gln Lys Gln Gly Ser Leu Ile Phe Ala Ser Asp Ile Asn Gln Gly
 370 375 380

GCG GGT GGT CTT TAT TTT GAG GGT AAT TTT ACA GTC TCT CCA AAT TCT 1259
 Ala Gly Gly Leu Tyr Phe Glu Gly Asn Phe Thr Val Ser Pro Asn Ser
 385 390 395 400

AAC CAA ACT TGG CAA GGA GCT GGC ATA CAT GTC AGT GAA AAT AGC ACC 1307
 Asn Gln Thr Trp Gln Gly Ala Gly Ile His Val Ser Glu Asn Ser Thr
 405 410 415

GTT ACT TGG AAA GTA AAT GGC GTG GAA CAT GAT CGA CTT TCT AAA ATT 1355
 Val Thr Trp Lys Val Asn Gly Val Glu His Asp Arg Leu Ser Lys Ile
 420 425 430

GGT AAA GGA ACA TTG CAC GTT CAA GCC AAA GGG GAA AAT AAA GGT TCG 1403
 Gly Lys Gly Thr Leu His Val Gln Ala Lys Gly Glu Asn Lys Gly Ser
 435 440 445

ATC AGC GTA GGC GAT GGT AAA GTC ATT TTG GAG CAG CAG GCA GAC GAT 1451
 Ile Ser Val Gly Asp Gly Lys Val Ile Leu Glu Gln Gln Ala Asp Asp
 450 455 460

CAA GGC AAC AAA CAA GCC TTT AGT GAA ATT GGC TTG GTT AGC GGC AGA 1499
 Gln Gly Asn Lys Gln Ala Phe Ser Glu Ile Gly Leu Val Ser Gly Arg
 465 470 475 480

GGG ACT GTT CAA TTA AAC GAT GAT AAA CAA TTT GAT ACC GAT AAA TTT 1547
 Gly Thr Val Gln Leu Asn Asp Asp Lys Gln Phe Asp Thr Asp Lys Phe
 485 490 495

TAT TTC GGC TTT CGT GGT CGC TTA GAT CTT AAC GGG CAT TCA TTA 1595
 Tyr Phe Gly Phe Arg Gly Arg Leu Asp Leu Asn Gly His Ser Leu
 500 505 510

ACC TTT AAA CGT ATC CAA AAT ACG GAC GAG GGG GCA ATG ATT GTG AAC 1643
 Thr Phe Lys Arg Ile Gln Asn Thr Asp Glu Gly Ala Met Ile Val Asn
 515 520 525

CAT AAT ACA ACT CAA GCC GCT AAT GTC ACT ATT ACT GGG AAC GAA AGC 1691
 His Asn Thr Thr Gln Ala Ala Asn Val Thr Ile Thr Gly Asn Glu Ser
 530 535 540

ATT GTT CTA CCT AAT GGA AAT AAT ATT AAT AAA CTT GAT TAC AGA AAA 1739
 Ile Val Leu Pro Asn Gly Asn Asn Ile Asn Lys Leu Asp Tyr Arg Lys
 545 550 555 560

 GAA ATT GCC TAC AAC GGT TGG TTT GGC GAA ACA GAT AAA AAT AAA CAC 1787
 Glu Ile Ala Tyr Asn Gly Trp Phe Gly Glu Thr Asp Lys Asn Lys His
 565 570 575

 AAT GGG CGA TTA AAC CTT ATT TAT AAA CCA ACC ACA GAA GAT CGT ACT 1835
 Asn Gly Arg Leu Asn Leu Ile Tyr Lys Pro Thr Thr Glu Asp Arg Thr
 580 585 590

 TTG CTA CTT TCA GGT ACA AAT TTA AAA GGC GAT ATT ACC CAA ACA 1883
 Leu Leu Leu Ser Gly Gly Thr Asn Leu Lys Gly Asp Ile Thr Gln Thr
 595 600 605

 AAA GGT AAA CTA TTT TTC AGC GGT AGA CCG ACA CCG CAC GCC TAC AAT 1931
 Lys Gly Lys Leu Phe Phe Ser Gly Arg Pro Thr Pro His Ala Tyr Asn
 610 615 620

 CAT TTA AAT AAA CGT TGG TCA GAA ATG GAA GGT ATA CCA CAA GGC GAA 1979
 His Leu Asn Lys Arg Trp Ser Glu Met Glu Gly Ile Pro Gln Gly Glu
 625 630 635 640

 ATT GTG TGG GAT CAC GAT TGG ATC AAC CGT ACA TTT AAA GCT GAA AAC 2027
 Ile Val Trp Asp His Asp Trp Ile Asn Arg Thr Phe Lys Ala Glu Asn
 645 650 655

 TTC CAA ATT AAA GGC GGA AGT GCG GTG GTT TCT CGC AAT GTT TCT TCA 2075
 Phe Gln Ile Lys Gly Gly Ser Ala Val Val Ser Arg Asn Val Ser Ser
 660 665 670

 ATT GAG GGA AAT TGG ACA GTC AGC AAT AAT GCA AAT GCC ACA TTT GGT 2123
 Ile Glu Gly Asn Trp Thr Val Ser Asn Asn Ala Asn Ala Thr Phe Gly
 675 680 685

 GTT GTG CCA AAT CAA CAA AAT ACC ATT TGC ACG CGT TCA GAT TGG ACA 2171
 Val Val Pro Asn Gln Gln Asn Thr Ile Cys Thr Arg Ser Asp Trp Thr
 690 695 700

 GGA TTA ACG ACT TGT CAA AAA GTG GAT TTA ACC GAT ACA AAA GTT ATT 2219
 Gly Leu Thr Thr Cys Gln Lys Val Asp Leu Thr Asp Thr Lys Val Ile
 705 710 715 720

 AAT TCT ATA CCA AAA ACA CAA ATC AAT GGC TCT ATT AAT TTA ACT GAT 2267
 Asn Ser Ile Pro Lys Thr Gln Ile Asn Gly Ser Ile Asn Leu Thr Asp
 725 730 735

 AAT GCA ACG GCG AAT GTT AAA GGT TTA GCA AAA CTT AAT GGC AAT GTC 2315
 Asn Ala Thr Ala Asn Val Lys Gly Leu Ala Lys Leu Asn Gly Asn Val
 740 745 750

 ACT TTA ACA AAT CAC AGC CAA TTT ACA TTA AGC AAC AAT GCC ACC CAA 2363
 Thr Leu Thr Asn His Ser Gln Phe Thr Leu Ser Asn Asn Ala Thr Gln
 755 760 765

 ATA GGC AAT ATT CGA CTT TCC GAC AAT TCA ACT GCA ACG GTG GAT AAT 2411
 Ile Gly Asn Ile Arg Leu Ser Asp Asn Ser Thr Ala Thr Val Asp Asn
 770 775 780

 GCA AAC TTG AAC GGT AAT GTG CAT TTA ACG GAT TCA GCT CAA TTT TCT 2459
 Ala Asn Leu Asn Gly Asn Val His Leu Thr Asp Ser Ala Gln Phe Ser
 785 790 795 800

 TTA AAA AAC AGC CAT TTT TCG CAC CAA ATT CAG GGA GAC AAA GGC ACA 2507

Leu Lys Asn Ser His Phe Ser His Gln Ile Gln Gly Asp Lys Gly Thr
 805 810 815

ACA GTG ACG TTG GAA AAT GCG ACT TGG ACA ATG CCT AGC GAT ACT ACA 2555
 Thr Val Thr Leu Glu Asn Ala Thr Trp Thr Met Pro Ser Asp Thr Thr
 820 825 830

TTG CAG AAT TTA ACG CTA AAT AAC AGT ACG ATC ACG TTA AAT TCA GCT 2603
 Leu Gln Asn Leu Thr Leu Asn Asn Ser Thr Ile Thr Leu Asn Ser Ala
 835 840 845

TAT TCA GCT AGC TCA AAC AAT ACG CCA CGT CGC CGT TCA TTA GAG ACG 2651
 Tyr Ser Ala Ser Ser Asn Asn Thr Pro Arg Arg Arg Ser Leu Glu Thr
 850 855 860

GAA ACA ACG CCA ACA TCG GCA GAA CAT CGT TTC AAC ACA TTG ACA GTA 2699
 Glu Thr Thr Pro Thr Ser Ala Glu His Arg Phe Asn Thr Leu Thr Val
 865 870 875 880

AAT GGT AAA TTG AGT GGG CAA GGC ACA TTC CAA TTT ACT TCA TCT TTA 2747
 Asn Gly Lys Leu Ser Gly Gln Gly Thr Phe Gln Phe Thr Ser Ser Leu
 885 890 895

TTT GGC TAT AAA AGC GAT AAA TTA AAA TTA TCC AAT GAC GCT GAG GGC 2795
 Phe Gly Tyr Lys Ser Asp Lys Leu Lys Leu Ser Asn Asp Ala Glu Gly
 900 905 910

GAT TAC ATA TTA TCT GTT CGC AAC ACA GGC AAA GAA CCC GAA ACC CTT 2843
 Asp Tyr Ile Leu Ser Val Arg Asn Thr Gly Lys Glu Pro Glu Thr Leu
 915 920 925

GAG CAA TTA ACT TTG GTT GAA AGC AAA GAT AAT CAA CCG TTA TCA GAT 2891
 Glu Gln Leu Thr Leu Val Glu Ser Lys Asp Asn Gln Pro Leu Ser Asp
 930 935 940

AAG CTC AAA TTT ACT TTA GAA AAT GAC CAC GTT GAT GCA GGT GCA TTA 2939
 Lys Leu Lys Phe Thr Leu Glu Asn Asp His Val Asp Ala Gly Ala Leu
 945 950 955 960

CGT TAT AAA TTA GTG AAG AAT GAT GGC GAA TTC CGC TTG CAT AAC CCA 2987
 Arg Tyr Lys Leu Val Lys Asn Asp Gly Glu Phe Arg Leu His Asn Pro
 965 970 975

ATA AAA GAG CAG GAA TTG CAC AAT GAT TTA GTA AGA GCA GAG CAA GCA 3035
 Ile Lys Glu Gln Glu Leu His Asn Asp Leu Val Arg Ala Glu Gln Ala
 980 985 990

GAA CGA ACA TTA GAA GCC AAA CAA GTT GAA CCG ACT GCT AAA ACA CAA 3083
 Glu Arg Thr Leu Glu Ala Lys Gln Val Glu Pro Thr Ala Lys Thr Gln
 995 1000 1005

ACA GGT GAG CCA AAA GTG CGG TCA AGA AGA GCA GCG AGA GCA GCG TTT 3131
 Thr Gly Glu Pro Lys Val Arg Ser Arg Arg Ala Ala Arg Ala Ala Phe
 1010 1015 1020

CCT GAT ACC CTG CCT GAT CAA AGC CTG TTA AAC GCA TTA GAA GCC AAA 3179
 Pro Asp Thr Leu Pro Asp Gln Ser Leu Leu Asn Ala Leu Glu Ala Lys
 1025 1030 1035 1040

CAA GCT GAA CTG ACT GCT GAA ACA CAA AAA AGT AAG GCA AAA ACA AAA 3227
 Gln Ala Glu Leu Thr Ala Glu Thr Gln Lys Ser Lys Ala Lys Thr Lys
 1045 1050 1055

AAA GTG CGG TCA AAA AGA GCA GTG TTT TCT GAT CCC CTG CTT GAT CAA 3275
 Lys Val Arg Ser Lys Arg Ala Val Phe Ser Asp Pro Leu Leu Asp Gln

1060	1065	1070	
AGC CTG TTC GCA TTA GAA GCC GCA CTT GAG GTT ATT GAT GCC CCA CAG 3323			
Ser Leu Phe Ala Leu Glu Ala Ala Leu Glu Val Ile Asp Ala Pro Gln			
1075	1080	1085	
CAA TCG GAA AAA GAT CGT CTA GCT CAA GAA GAA GCG GAA AAA CAA CGC 3371			
Gln Ser Glu Lys Asp Arg Leu Ala Gln Glu Ala Glu Lys Gln Arg			
1090	1095	1100	
AAA CAA AAA GAC TTG ATC AGC CGT TAT TCA AAT AGT GCG TTA TCA GAA 3419			
Lys Gln Lys Asp Leu Ile Ser Arg Tyr Ser Asn Ser Ala Leu Ser Glu			
1105	1110	1115	1120
TTA TCT GCA ACA GTA AAT AGT ATG CTT TCT GTT CAA GAT GAA TTA GAT 3467			
Leu Ser Ala Thr Val Asn Ser Met Leu Ser Val Gln Asp Glu Leu Asp			
1125	1130	1135	
CGT CTT TTT GTA GAT CAA GCA CAA TCT GCC GTG TGG ACA AAT ATC GCA 3515			
Arg Leu Phe Val Asp Gln Ala Gln Ser Ala Val Trp Thr Asn Ile Ala			
1140	1145	1150	
CAG GAT AAA AGA CGC TAT GAT TCT GAT GCG TTC CGT GCT TAT CAG CAG 3563			
Gln Asp Lys Arg Arg Tyr Asp Ser Asp Ala Phe Arg Ala Tyr Gln Gln			
1155	1160	1165	
CAG AAA ACG AAC TTA CGT CAA ATT GGG GTG CAA AAA GCC TTA GCT AAT 3611			
Gln Lys Thr Asn Leu Arg Gln Ile Gly Val Gln Lys Ala Leu Ala Asn			
1170	1175	1180	
GGA CGA ATT GGG GCA GTT TTC TCG CAT AGC CGT TCA GAT AAT ACC TTT 3659			
Gly Arg Ile Gly Ala Val Phe Ser His Ser Arg Ser Asp Asn Thr Phe			
1185	1190	1195	1200
GAT GAA CAG GTT AAA AAT CAC GCG ACA TTA ACG ATG ATG TCG GGT TTT 3707			
Asp Glu Gln Val Lys Asn His Ala Thr Leu Thr Met Met Ser Gly Phe			
1205	1210	1215	
GCC CAA TAT CAA TGG GGC GAT TTA CAA TTT GGT GTA AAC GTG GGA ACG 3755			
Ala Gln Tyr Gln Trp Gly Asp Leu Gln Phe Gly Val Asn Val Gly Thr			
1220	1225	1230	
GGA ATC AGT GCG AGT AAA ATG GCT GAA GAA CAA AGC CGA AAA ATT CAT 3803			
Gly Ile Ser Ala Ser Lys Met Ala Glu Glu Gln Ser Arg Lys Ile His			
1235	1240	1245	
CGA AAA GCG ATA AAT TAT GGC GTG AAT GCA AGT TAT CAG TTC CGT TTA 3851			
Arg Lys Ala Ile Asn Tyr Gly Val Asn Ala Ser Tyr Gln Phe Arg Leu			
1250	1255	1260	
GGG CAA TTG GGC ATT CAG CCT TAT TTT GGA GTT AAT CGC TAT TTT ATT. 3899			
Gly Gln Leu Gly Ile Gln Pro Tyr Phe Gly Val Asn Arg Tyr Phe Ile			
1265	1270	1275	1280
GAA CGT GAA AAT TAT CAA TCT GAG GAA GTG AGA GTG AAA ACG CCT AGC 3947			
Glu Arg Glu Asn Tyr Gln Ser Glu Glu Val Arg Val Lys Thr Pro Ser			
1285	1290	1295	
CTT GCA TTT AAT CGC TAT AAT GCT GGC ATT CGA GTT GAT TAT ACA TTT 3995			
Leu Ala Phe Asn Arg Tyr Asn Ala Gly Ile Arg Val Asp Tyr Thr Phe			
1300	1305	1310	
ACT CCG ACA GAT AAT ATC AGC GTT AAG CCT TAT TTC TTC GTC AAT TAT 4043			
Thr Pro Thr Asp Asn Ile Ser Val Lys Pro Tyr Phe Phe Val Asn Tyr			
1315	1320	1325	

GTT GAT GTT TCA AAC GCT AAC GTA CAA ACC ACG GTA AAT CTC ACG GTG 4091
 Val Asp Val Ser Asn Ala Asn Val Gln Thr Thr Val Asn Leu Thr Val
 1330 1335 1340

 TTG CAA CAA CCA TTT GGA CGT TAT TGG CAA AAA GAA GTG GGA TTA AAG 4139
 Leu Gln Gln Pro Phe Gly Arg Tyr Trp Gln Lys Glu Val Gly Leu Lys
 1345 1350 1355 1360

 GCA GAA ATT TTA CAT TTC CAA ATT TCC GCT TTT ATC TCA AAA TCT CAA 4187
 Ala Glu Ile Leu His Phe Gln Ile Ser Ala Phe Ile Ser Lys Ser Gln
 1365 1370 1375

 GGT TCA CAA CTC GGC AAA CAG CAA AAT GTG GGC GTG AAA TTG GGC TAT 4235
 Gly Ser Gln Leu Gly Lys Gln Gln Asn Val Gly Val Lys Leu Gly Tyr
 1380 1385 1390

 CGT TGG TAAAAATCA ACATAATTT ATCGTTTATT GATAAACAAAG GTGGGTCAGA 4290
 Arg Trp

 TCAGATCCCA CCTTTTTAT TCCAATAAT 4319

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1394 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Lys Thr Val Phe Arg Leu Asn Phe Leu Thr Ala Cys Ile Ser
 1 5 10 15

 Leu Gly Ile Val Ser Gln Ala Trp Ala Gly His Thr Tyr Phe Gly Ile
 20 25 30

 Asp Tyr Gln Tyr Tyr Arg Asp Phe Ala Glu Asn Lys Gly Lys Phe Thr
 35 40 45

 Val Gly Ala Gln Asn Ile Lys Val Tyr Asn Lys Gln Gly Gln Leu Val
 50 55 60

 Gly Thr Ser Met Thr Lys Ala Pro Met Ile Asp Phe Ser Val Val Ser
 65 70 75 80

 Arg Asn Gly Val Ala Ala Leu Val Glu Asn Gln Tyr Ile Val Ser Val
 85 90 95

 Ala His Asn Val Gly Tyr Thr Asp Val Asp Phe Gly Ala Glu Gly Asn
 100 105 110

 Asn Pro Asp Gln His Arg Phe Thr Tyr Lys Ile Val Lys Arg Asn Asn
 115 120 125

 Tyr Lys Lys Asp Asn Leu His Pro Tyr Glu Asp Asp Tyr His Asn Pro
 130 135 140

 Arg Leu His Lys Phe Val Thr Glu Ala Ala Pro Ile Asp Met Thr Ser
 145 150 155 160

 Asn Met Asn Gly Ser Thr Tyr Ser Asp Arg Thr Lys Tyr Pro Glu Arg
 165 170 175

Val Arg Ile Gly Ser Gly Arg Gln Phe Trp Arg Asn Asp Gln Asp Lys
180 185 190

Gly Asp Gln Val Ala Gly Ala Tyr His Tyr Leu Thr Ala Gly Asn Thr
195 200 205

His Asn Gln Arg Gly Ala Gly Asn Gly Tyr Ser Tyr Leu Gly Gly Asp
210 215 220

Val Arg Lys Ala Gly Glu Tyr Gly Pro Leu Pro Ile Ala Gly Ser Lys
225 230 235 240

Gly Asp Ser Gly Ser Pro Met Phe Ile Tyr Asp Ala Glu Lys Gln Lys
245 250 255

Trp Leu Ile Asn Gly Ile Leu Arg Glu Gly Asn Pro Phe Glu Gly Lys
260 265 270

Glu Asn Gly Phe Gln Leu Val Arg Lys Ser Tyr Phe Asp Glu Ile Phe
275 280 285

Glu Arg Asp Leu His Thr Ser Leu Tyr Thr Arg Ala Gly Asn Gly Val
290 295 300

Tyr Thr Ile Ser Gly Asn Asp Asn Gly Gln Gly Ser Ile Thr Gln Lys
305 310 315 320

Ser Gly Ile Pro Ser Glu Ile Lys Ile Thr Leu Ala Asn Met Ser Leu
325 330 335

Pro Leu Lys Glu Lys Asp Lys Val His Asn Pro Arg Tyr Asp Gly Pro
340 345 350

Asn Ile Tyr Ser Pro Arg Leu Asn Asn Gly Glu Thr Leu Tyr Phe Met
355 360 365

Asp Gln Lys Gln Gly Ser Leu Ile Phe Ala Ser Asp Ile Asn Gln Gly
370 375 380

Ala Gly Gly Leu Tyr Phe Glu Gly Asn Phe Thr Val Ser Pro Asn Ser
385 390 395 400

Asn Gln Thr Trp Gln Gly Ala Gly Ile His Val Ser Glu Asn Ser Thr
405 410 415

Val Thr Trp Lys Val Asn Gly Val Glu His Asp Arg Leu Ser Lys Ile
420 425 430

Gly Lys Gly Thr Leu His Val Gln Ala Lys Gly Glu Asn Lys Gly Ser
435 440 445

Ile Ser Val Gly Asp Gly Lys Val Ile Leu Glu Gln Gln Ala Asp Asp
450 455 460

Gln Gly Asn Lys Gln Ala Phe Ser Glu Ile Gly Leu Val Ser Gly Arg
465 470 475 480

Gly Thr Val Gln Leu Asn Asp Asp Lys Gln Phe Asp Thr Asp Lys Phe
485 490 495

Tyr Phe Gly Phe Arg Gly Arg Leu Asp Leu Asn Gly His Ser Leu
500 505 510

Thr Phe Lys Arg Ile Gln Asn Thr Asp Glu Gly Ala Met Ile Val Asn
515 520 525

His Asn Thr Thr Gln Ala Ala Asn Val Thr Ile Thr Gly Asn Glu Ser

530

535

540

Ile Val Leu Pro Asn Gly Asn Asn Ile Asn Lys Leu Asp Tyr Arg Lys
 545 550 555 560

Glu Ile Ala Tyr Asn Gly Trp Phe Gly Glu Thr Asp Lys Asn Lys His
 565 570 575

Asn Gly Arg Leu Asn Leu Ile Tyr Lys Pro Thr Thr Glu Asp Arg Thr
 580 585 590

Leu Leu Leu Ser Gly Gly Thr Asn Leu Lys Gly Asp Ile Thr Gln Thr
 595 600 605

Lys Gly Lys Leu Phe Phe Ser Gly Arg Pro Thr Pro His Ala Tyr Asn
 610 615 620

His Leu Asn Lys Arg Trp Ser Glu Met Glu Gly Ile Pro Gln Gly Glu
 625 630 635 640

Ile Val Trp Asp His Asp Trp Ile Asn Arg Thr Phe Lys Ala Glu Asn
 645 650 655

Phe Gln Ile Lys Gly Gly Ser Ala Val Val Ser Arg Asn Val Ser Ser
 660 665 670

Ile Glu Gly Asn Trp Thr Val Ser Asn Asn Ala Asn Ala Thr Phe Gly
 675 680 685

Val Val Pro Asn Gln Gln Asn Thr Ile Cys Thr Arg Ser Asp Trp Thr
 690 695 700

Gly Leu Thr Thr Cys Gln Lys Val Asp Leu Thr Asp Thr Lys Val Ile
 705 710 715 720

Asn Ser Ile Pro Lys Thr Gln Ile Asn Gly Ser Ile Asn Leu Thr Asp
 725 730 735

Asn Ala Thr Ala Asn Val Lys Gly Leu Ala Lys Leu Asn Gly Asn Val
 740 745 750

Thr Leu Thr Asn His Ser Gln Phe Thr Leu Ser Asn Asn Ala Thr Gln
 755 760 765

Ile Gly Asn Ile Arg Leu Ser Asp Asn Ser Thr Ala Thr Val Asp Asn
 770 775 780

Ala Asn Leu Asn Gly Asn Val His Leu Thr Asp Ser Ala Gln Phe Ser
 785 790 795 800

Leu Lys Asn Ser His Phe Ser His Gln Ile Gln Gly Asp Lys Gly Thr
 805 810 815

Thr Val Thr Leu Glu Asn Ala Thr Trp Thr Met Pro Ser Asp Thr Thr
 820 825 830

Leu Gln Asn Leu Thr Leu Asn Asn Ser Thr Ile Thr Leu Asn Ser Ala
 835 840 845

Tyr Ser Ala Ser Ser Asn Asn Thr Pro Arg Arg Arg Ser Leu Glu Thr
 850 855 860

Glu Thr Thr Pro Thr Ser Ala Glu His Arg Phe Asn Thr Leu Thr Val
 865 870 875 880

Asn Gly Lys Leu Ser Gly Gln Gly Thr Phe Gln Phe Thr Ser Ser Leu
 885 890 895

Phe Gly Tyr Lys Ser Asp Lys Leu Lys Leu Ser Asn Asp Ala Glu Gly
900 905 910

Asp Tyr Ile Leu Ser Val Arg Asn Thr Gly Lys Glu Pro Glu Thr Leu
915 920 925

Glu Gln Leu Thr Leu Val Glu Ser Lys Asp Asn Gln Pro Leu Ser Asp
930 935 940

Lys Leu Lys Phe Thr Leu Glu Asn Asp His Val Asp Ala Gly Ala Leu
945 950 955 960

Arg Tyr Lys Leu Val Lys Asn Asp Gly Glu Phe Arg Leu His Asn Pro
965 970 975

Ile Lys Glu Gln Glu Leu His Asn Asp Leu Val Arg Ala Gln Ala
980 985 990

Glu Arg Thr Leu Glu Ala Lys Gln Val Glu Pro Thr Ala Lys Thr Gln
995 1000 1005

Thr Gly Glu Pro Lys Val Arg Ser Arg Arg Ala Ala Arg Ala Ala Phe
1010 1015 1020

Pro Asp Thr Leu Pro Asp Gln Ser Leu Leu Asn Ala Leu Glu Ala Lys
1025 1030 1035 1040

Gln Ala Glu Leu Thr Ala Glu Thr Gln Lys Ser Lys Ala Lys Thr Lys
1045 1050 1055

Lys Val Arg Ser Lys Arg Ala Val Phe Ser Asp Pro Leu Leu Asp Gln
1060 1065 1070

Ser Leu Phe Ala Leu Glu Ala Ala Leu Glu Val Ile Asp Ala Pro Gln
1075 1080 1085

Gln Ser Glu Lys Asp Arg Leu Ala Gln Glu Glu Ala Glu Lys Gln Arg
1090 1095 1100

Lys Gln Lys Asp Leu Ile Ser Arg Tyr Ser Asn Ser Ala Leu Ser Glu
1105 1110 1115 1120

Leu Ser Ala Thr Val Asn Ser Met Leu Ser Val Gln Asp Glu Leu Asp
1125 1130 1135

Arg Leu Phe Val Asp Gln Ala Gln Ser Ala Val Trp Thr Asn Ile Ala
1140 1145 1150

Gln Asp Lys Arg Arg Tyr Asp Ser Asp Ala Phe Arg Ala Tyr Gln Gln
1155 1160 1165

Gln Lys Thr Asn Leu Arg Gln Ile Gly Val Gln Lys Ala Leu Ala Asn
1170 1175 1180

Gly Arg Ile Gly Ala Val Phe Ser His Ser Arg Ser Asp Asn Thr Phe
1185 1190 1195 1200

Asp Glu Gln Val Lys Asn His Ala Thr Leu Thr Met Met Ser Gly Phe
1205 1210 1215

Ala Gln Tyr Gln Trp Gly Asp Leu Gln Phe Gly Val Asn Val Gly Thr
1220 1225 1230

Gly Ile Ser Ala Ser Lys Met Ala Glu Glu Gln Ser Arg Lys Ile His
1235 1240 1245

Arg Lys Ala Ile Asn Tyr Gly Val Asn Ala Ser Tyr Gln Phe Arg Leu

1250	1255	1260	
Gly Gln Leu Gly Ile Gln Pro Tyr Phe Gly Val Asn Arg Tyr Phe Ile			
1265	1270	1275	1280
Glu Arg Glu Asn Tyr Gln Ser Glu Glu Val Arg Val Lys Thr Pro Ser			
1285	1290	1295	
Leu Ala Phe Asn Arg Tyr Asn Ala Gly Ile Arg Val Asp Tyr Thr Phe			
1300	1305	1310	
Thr Pro Thr Asp Asn Ile Ser Val Lys Pro Tyr Phe Phe Val Asn Tyr			
1315	1320	1325	
Val Asp Val Ser Asn Ala Asn Val Gln Thr Thr Val Asn Leu Thr Val			
1330	1335	1340	
Leu Gln Gln Pro Phe Gly Arg Tyr Trp Gln Lys Glu Val Gly Leu Lys			
1345	1350	1355	1360
Ala Glu Ile Leu His Phe Gln Ile Ser Ala Phe Ile Ser Lys Ser Gln			
1365	1370	1375	
Gly Ser Gln Leu Gly Lys Gln Gln Asn Val Gly Val Lys Leu Gly Tyr			
1380	1385	1390	
Arg Trp			

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1541 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Leu Asn Lys Lys Phe Lys Leu Asn Phe Ile Ala Leu Thr Val Ala
1 5 10 15

Tyr Ala Leu Thr Pro Tyr Thr Glu Ala Ala Leu Val Arg Asp Asp Val
20 25 30

Asp Tyr Gln Ile Phe Arg Asp Phe Ala Glu Asn Lys Gly Lys Phe Ser
35 40 45

Val Gly Ala Thr Asn Val Leu Val Lys Asp Lys Asn Asn Lys Asp Leu
50 55 60

Gly Thr Ala Leu Pro Asn Gly Ile Pro Met Ile Asp Phe Ser Val Val
65 70 75 80

Asp Val Asp Lys Arg Ile Ala Thr Leu Ile Asn Pro Gln Tyr Val Val
85 90 95

Gly Val Lys His Val Ser Asn Gly Val Ser Glu Leu His Phe Gly Asn
 100 105 110

Leu Asn Gly Asn Met Asn Asn Gly Asn Ala Lys Ala His Arg Asp Val
115 120 125

Ser Ser Glu Glu Asn Arg Tyr Phe Ser Val Glu Lys Asn Glu Tyr Pro
 130 135 140

Thr Lys Leu Asn Gly Lys Thr Val Thr Thr Glu Asp Gln Thr Gln Lys
145 150 155 160

Arg Arg Glu Asp Tyr Tyr Met Pro Arg Leu Asp Lys Phe Val Thr Glu
165 170 175

Val Ala Pro Ile Glu Ala Ser Thr Ala Ser Ser Asp Ala Gly Thr Tyr
180 185 190

Asn Asp Gln Asn Lys Tyr Pro Ala Phe Val Arg Leu Gly Ser Gly Ser
195 200 205

Gln Phe Ile Tyr Lys Lys Gly Asp Asn Tyr Ser Leu Ile Leu Asn Asn
210 215 220

His Glu Val Gly Gly Asn Asn Leu Lys Leu Val Gly Asp Ala Tyr Thr
225 230 235 240

Tyr Gly Ile Ala Gly Thr Pro Tyr Lys Val Asn His Glu Asn Asn Gly
245 250 255

Leu Ile Gly Phe Gly Asn Ser Lys Glu Glu His Ser Asp Pro Lys Gly
260 265 270

Ile Leu Ser Gln Asp Pro Leu Thr Asn Tyr Ala Val Leu Gly Asp Ser
275 280 285

Gly Ser Pro Leu Phe Val Tyr Asp Arg Glu Lys Gly Lys Trp Leu Phe
290 295 300

Leu Gly Ser Tyr Asp Phe Trp Ala Gly Tyr Asn Lys Lys Ser Trp Gln
305 310 315 320

Glu Trp Asn Ile Tyr Lys Ser Gln Phe Thr Lys Asp Val Leu Asn Lys
325 330 335

Asp Ser Ala Gly Ser Leu Ile Gly Ser Lys Thr Asp Tyr Ser Trp Ser
340 345 350

Ser Asn Gly Lys Thr Ser Thr Ile Thr Gly Gly Glu Lys Ser Leu Asn
355 360 365

Val Asp Leu Ala Asp Gly Lys Asp Lys Pro Asn His Gly Lys Ser Val
370 375 380

Thr Phe Glu Gly Ser Gly Thr Leu Thr Leu Asn Asn Asn Ile Asp Gln
385 390 395 400

Gly Ala Gly Gly Leu Phe Phe Glu Gly Asp Tyr Glu Val Lys Gly Thr
405 410 415

Ser Asp Asn Thr Thr Trp Lys Gly Ala Gly Val Ser Val Ala Glu Gly
420 425 430

Lys Thr Val Thr Trp Lys Val His Asn Pro Gln Tyr Asp Arg Leu Ala
435 440 445

Lys Ile Gly Lys Gly Thr Leu Ile Val Glu Gly Thr Gly Asp Asn Lys
450 455 460

Gly Ser Leu Lys Val Gly Asp Gly Thr Val Ile Leu Lys Gln Gln Thr
465 470 475 480

Asn Gly Ser Gly Gln His Ala Phe Ala Ser Val Gly Ile Val Ser Gly
485 490 495

Arg Ser Thr Leu Val Leu Asn Asp Asp Lys Gln Val Asp Pro Asn Ser

500 505 510
Ile Tyr Phe Gly Phe Arg Gly Gly Arg Leu Asp Leu Asn Gly Asn Ser
515 520 525
Leu Thr Phe Asp His Ile Arg Asn Ile Asp Asp Gly Ala Arg Leu Val
530 535 540
Asn His Asn Met Thr Asn Ala Ser Asn Ile Thr Ile Thr Gly Glu Ser
545 550 555 560
Leu Ile Thr Asp Pro Asn Thr Ile Thr Pro Tyr Asn Ile Asp Ala Pro
565 570 575
Asp Glu Asp Asn Pro Tyr Ala Phe Arg Arg Ile Lys Asp Gly Gly Gln
580 585 590
Leu Tyr Leu Asn Leu Glu Asn Tyr Thr Tyr Tyr Ala Leu Arg Lys Gly
595 600 605
Ala Ser Thr Arg Ser Glu Leu Pro Lys Asn Ser Gly Glu Ser Asn Glu
610 615 620
Asn Trp Leu Tyr Met Gly Lys Thr Ser Asp Glu Ala Lys Arg Asn Val
625 630 635 640
Met Asn His Ile Asn Asn Glu Arg Met Asn Gly Phe Asn Gly Tyr Phe
645 650 655
Gly Glu Glu Glu Gly Lys Asn Asn Gly Asn Leu Asn Val Thr Phe Lys
660 665 670
Gly Lys Ser Glu Gln Asn Arg Phe Leu Leu Thr Gly Gly Thr Asn Leu
675 680 685
Asn Gly Asp Leu Thr Val Glu Lys Gly Thr Leu Phe Leu Ser Gly Arg
690 695 700
Pro Thr Pro His Ala Arg Asp Ile Ala Gly Ile Ser Ser Thr Lys Lys
705 710 715 720
Asp Pro His Phe Ala Glu Asn Asn Glu Val Val Val Glu Asp Asp Trp
725 730 735
Ile Asn Arg Asn Phe Lys Ala Thr Thr Met Asn Val Thr Gly Asn Ala
740 745 750
Ser Leu Tyr Ser Gly Arg Asn Val Ala Asn Ile Thr Ser Asn Ile Thr
755 760 765
Ala Ser Asn Lys Ala Gln Val His Ile Gly Tyr Lys Thr Gly Asp Thr
770 775 780
Val Cys Val Arg Ser Asp Tyr Thr Gly Tyr Val Thr Cys Thr Thr Asp
785 790 795 800
Lys Leu Ser Asp Lys Ala Leu Asn Ser Phe Asn Pro Thr Asn Leu Arg
805 810 815
Gly Asn Val Asn Leu Thr Glu Ser Ala Asn Phe Val Leu Gly Lys Ala
820 825 830
Asn Leu Phe Gly Thr Ile Gln Ser Arg Gly Asn Ser Gln Val Arg Leu
835 840 845
Thr Glu Asn Ser His Trp His Leu Thr Gly Asn Ser Asp Val His Gln
850 855 860

Leu Asp Leu Ala Asn Gly His Ile His Leu Asn Ser Ala Asp Asn Ser
865 870 875 880
Asn Asn Val Thr Lys Tyr Asn Thr Leu Thr Val Asn Ser Leu Ser Gly
885 890 895
Asn Gly Ser Phe Tyr Tyr Leu Thr Asp Leu Ser Asn Lys Gln Gly Asp
900 905 910
Lys Val Val Val Thr Lys Ser Ala Thr Gly Asn Phe Thr Leu Gln Val
915 920 925
Ala Asp Lys Thr Gly Glu Pro Asn His Asn Glu Leu Thr Leu Phe Asp
930 935 940
Ala Ser Lys Ala Gln Arg Asp His Leu Asn Val Ser Leu Val Gly Asn
945 950 955 960
Thr Val Asp Leu Gly Ala Trp Lys Tyr Lys Leu Arg Asn Val Asn Gly
965 970 975
Arg Tyr Asp Leu Tyr Asn Pro Glu Val Glu Lys Arg Asn Gln Thr Val
980 985 990
Asp Thr Thr Asn Ile Thr Thr Pro Asn Asn Ile Gln Ala Asp Val Pro
995 1000 1005
Ser Val Pro Ser Asn Asn Glu Glu Ile Ala Arg Val Asp Glu Ala Pro
1010 1015 1020
Val Pro Pro Pro Ala Pro Ala Thr Pro Ser Glu Thr Thr Glu Thr Val
1025 1030 1035 1040
Ala Glu Asn Ser Lys Gln Glu Ser Lys Thr Val Glu Lys Asn Glu Gln
1045 1050 1055
Asp Ala Thr Glu Thr Thr Ala Gln Asn Arg Glu Val Ala Lys Glu Ala
1060 1065 1070
Lys Ser Asn Val Lys Ala Asn Thr Gln Thr Asn Glu Val Ala Gln Ser
1075 1080 1085
Gly Ser Glu Thr Lys Glu Thr Gln Thr Glu Thr Lys Glu Thr Ala
1090 1095 1100
Thr Val Glu Lys Glu Glu Lys Ala Lys Val Glu Thr Glu Lys Thr Gln
1105 1110 1115 1120
Glu Val Pro Lys Val Thr Ser Gln Val Ser Pro Lys Gln Glu Gln Ser
1125 1130 1135
Glu Thr Val Gln Pro Gln Ala Glu Pro Ala Arg Glu Asn Asp Pro Thr
1140 1145 1150
Val Asn Ile Lys Glu Pro Gln Ser Gln Thr Asn Thr Thr Ala Asp Thr
1155 1160 1165
Glu Gln Pro Ala Lys Glu Thr Ser Ser Asn Val Glu Gln Pro Val Thr
1170 1175 1180
Glu Ser Thr Thr Val Asn Thr Gly Asn Ser Val Val Glu Asn Pro Glu
1185 1190 1195 1200
Asn Thr Thr Pro Ala Thr Thr Gln Pro Thr Val Asn Ser Glu Ser Ser
1205 1210 1215
Asn Lys Pro Lys Asn Arg His Arg Arg Ser Val Arg Ser Val Pro His

1220	1225	1230
Asn Val Glu Pro Ala Thr Thr Ser Ser Asn Asp Arg Ser Thr Val Ala		
1235	1240	1245
Leu Cys Asp Leu Thr Ser Thr Asn Thr Asn Ala Val Leu Ser Asp Ala		
1250	1255	1260
Arg Ala Lys Ala Gln Phe Val Ala Leu Asn Val Gly Lys Ala Val Ser		
1265	1270	1275
Gln His Ile Ser Gln Leu Glu Met Asn Asn Glu Gly Gln Tyr Asn Val		
1285	1290	1295
Trp Val Ser Asn Thr Ser Met Asn Lys Asn Tyr Ser Ser Gln Tyr		
1300	1305	1310
Arg Arg Phe Ser Ser Lys Ser Thr Gln Thr Gln Leu Gly Trp Asp Gln		
1315	1320	1325
Thr Ile Ser Asn Asn Val Gln Leu Gly Gly Val Phe Thr Tyr Val Arg		
1330	1335	1340
Asn Ser Asn Asn Phe Asp Lys Ala Thr Ser Lys Asn Thr Leu Ala Gln		
1345	1350	1355
Val Asn Phe Tyr Ser Lys Tyr Tyr Ala Asp Asn His Trp Tyr Leu Gly		
1365	1370	1375
Ile Asp Leu Gly Tyr Gly Lys Phe Gln Ser Lys Leu Gln Thr Asn His		
1380	1385	1390
Asn Ala Lys Phe Ala Arg His Thr Ala Gln Phe Gly Leu Thr Ala Gly		
1395	1400	1405
Lys Ala Phe Asn Leu Gly Asn Phe Gly Ile Thr Pro Ile Val Gly Val		
1410	1415	1420
Arg Tyr Ser Tyr Leu Ser Asn Ala Asp Phe Ala Asp Gln Ala Arg		
1425	1430	1435
Ile Lys Val Asn Pro Ile Ser Val Lys Thr Ala Phe Ala Gln Val Asp		
1445	1450	1455
Leu Ser Tyr Thr Tyr His Leu Gly Glu Phe Ser Val Thr Pro Ile Leu		
1460	1465	1470
Ser Ala Arg Tyr Asp Ala Asn Gln Gly Ser Gly Lys Ile Asn Val Asn		
1475	1480	1485
Gly Tyr Asp Phe Ala Tyr Asn Val Glu Asn Gln Gln Gln Tyr Asn Ala		
1490	1495	1500
Gly Leu Lys Leu Lys Tyr His Asn Val Lys Leu Ser Leu Ile Gly Gly		
1505	1510	1515
Leu Thr Lys Ala Lys Gln Ala Glu Lys Gln Lys Thr Ala Glu Leu Lys		
1525	1530	1535
Leu Ser Phe Ser Phe		
1540		

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1545 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Leu Asn Lys Lys Phe Lys Leu Asn Phe Ile Ala Leu Thr Val Ala
1 5 10 15

Tyr Ala Leu Thr Pro Tyr Thr Glu Ala Ala Leu Val Arg Asp Asp Val
20 25 30

Asp Tyr Gln Ile Phe Arg Asp Phe Ala Glu Asn Lys Gly Lys Phe Ser
35 40 45

Val Gly Ala Thr Asn Val Glu Val Arg Asp Lys Asn Asn Arg Pro Leu
50 55 60

Gly Asn Val Leu Pro Asn Gly Ile Pro Met Ile Asp Phe Ser Val Val
65 70 75 80

Asp Val Asp Lys Arg Ile Ala Thr Leu Val Asn Pro Gln Tyr Val Val
85 90 95

Gly Val Lys His Val Ser Asn Gly Val Ser Glu Leu His Phe Gly Asn
100 105 110

Leu Asn Gly Asn Met Asn Asn Gly Asn Ala Lys Ala His Arg Asp Val
115 120 125

Ser Ser Glu Glu Asn Arg Tyr Tyr Thr Val Glu Lys Asn Glu Tyr Pro
130 135 140

Thr Lys Leu Asn Gly Lys Ala Val Thr Thr Glu Asp Gln Ala Gln Lys
145 150 155 160

Arg Arg Glu Asp Tyr Tyr Met Pro Arg Leu Asp Lys Phe Val Thr Glu
165 170 175

Val Ala Pro Ile Glu Ala Ser Thr Asp Ser Ser Thr Ala Gly Thr Tyr
180 185 190

Asn Asn Lys Asp Lys Tyr Pro Tyr Phe Val Arg Leu Gly Ser Gly Thr
195 200 205

Gln Phe Ile Tyr Glu Asn Gly Thr Arg Tyr Glu Leu Trp Leu Gly Lys
210 215 220

Glu Gly Gln Lys Ser Asp Ala Gly Gly Tyr Asn Leu Lys Leu Val Gly
225 230 235 240

Asn Ala Tyr Thr Tyr Gly Ile Ala Gly Thr Pro Tyr Glu Val Asn His
245 250 255

Glu Asn Asp Gly Leu Ile Gly Phe Gly Asn Ser Asn Asn Glu Tyr Ile
260 265 270

Asn Pro Lys Glu Ile Leu Ser Lys Lys Pro Leu Thr Asn Tyr Ala Val
275 280 285

Leu Gly Asp Ser Gly Ser Pro Leu Phe Val Tyr Asp Arg Glu Lys Gly
290 295 300

Lys Trp Leu Phe Leu Gly Ser Tyr Asp Tyr Trp Ala Gly Tyr Asn Lys
305 310 315 320

Lys Ser Trp Gln Glu Trp Asn Ile Tyr Lys Pro Glu Phe Ala Glu Lys
325 330 335

Ile Tyr Glu Gln Tyr Ser Ala Gly Ser Leu Ile Gly Ser Lys Thr Asp
340 345 350

Tyr Ser Trp Ser Ser Asn Gly Lys Thr Ser Thr Ile Thr Gly Gly Glu
355 360 365

Lys Ser Leu Asn Val Asp Leu Ala Asp Gly Lys Asp Lys Pro Asn His
370 375 380

Gly Lys Ser Val Thr Phe Glu Gly Ser Gly Thr Leu Thr Leu Asn Asn
385 390 395 400

Asn Ile Asp Gln Gly Ala Gly Gly Leu Phe Phe Glu Gly Asp Tyr Glu
405 410 415

Val Lys Gly Thr Ser Asp Asn Thr Thr Trp Lys Gly Ala Gly Val Ser
420 425 430

Val Ala Glu Gly Lys Thr Val Thr Trp Lys Val His Asn Pro Gln Tyr
435 440 445

Asp Arg Leu Ala Lys Ile Gly Lys Gly Thr Leu Ile Val Glu Gly Thr
450 455 460

Gly Asp Asn Lys Gly Ser Leu Lys Val Gly Asp Gly Thr Val Ile Leu
465 470 475 480

Lys Gln Gln Thr Asn Gly Ser Gly Gln His Ala Phe Ala Ser Val Gly
485 490 495

Ile Val Ser Gly Arg Ser Thr Leu Val Leu Asn Asp Asp Lys Gln Val
500 505 510

Asp Pro Asn Ser Ile Tyr Phe Gly Phe Arg Gly Arg Leu Asp Leu
515 520 525

Asn Gly Asn Ser Leu Thr Phe Asp His Ile Arg Asn Ile Asp Glu Gly
530 535 540

Ala Arg Leu Val Asn His Ser Thr Ser Lys His Ser Thr Val Thr Ile
545 550 555 560

Thr Gly Asp Asn Leu Ile Thr Asp Pro Asn Asn Val Ser Ile Tyr Tyr
565 570 575

Val Lys Pro Leu Glu Asp Asp Asn Pro Tyr Ala Ile Arg Gln Ile Lys
580 585 590

Tyr Gly Tyr Gln Leu Tyr Phe Asn Glu Glu Asn Arg Thr Tyr Tyr Ala
595 600 605

Leu Lys Lys Asp Ala Ser Ile Arg Ser Glu Phe Pro Gln Asn Arg Gly
610 615 620

Glu Ser Asn Asn Ser Trp Leu Tyr Met Gly Thr Glu Lys Ala Asp Ala
625 630 635 640

Gln Lys Asn Ala Met Asn His Ile Asn Asn Glu Arg Met Asn Gly Phe
645 650 655

Asn Gly Tyr Phe Gly Glu Glu Gly Lys Asn Asn Gly Asn Leu Asn
660 665 670

Val Thr Phe Lys Gly Lys Ser Glu Gln Asn Arg Phe Leu Leu Thr Gly

675	680	685	
Gly Thr Asn Leu Asn Gly Asp	Leu Asn Val Gln Gln	Gly Thr Leu Phe	
690	695	700	
Leu Ser Gly Arg Pro Thr Pro His Ala Arg Asp	Ile Ala Gly Ile Ser		
705	710	715	720
Ser Thr Lys Lys Asp Ser His Phe Ser Glu Asn Asn Glu Val Val Val			
725	730	735	
Glu Asp Asp Trp Ile Asn Arg Asn Phe Lys Ala Thr Asn Ile Asn Val			
740	745	750	
Thr Asn Asn Ala Thr Leu Tyr Ser Gly Arg Asn Val Glu Ser Ile Thr			
755	760	765	
Ser Asn Ile Thr Ala Ser Asn Asn Ala Lys Val His Ile Gly Tyr Lys			
770	775	780	
Ala Gly Asp Thr Val Cys Val Arg Ser Asp Tyr Thr Gly Tyr Val Thr			
785	790	795	800
Cys Thr Thr Asp Lys Leu Ser Asp Lys Ala Leu Asn Ser Phe Asn Pro			
805	810	815	
Thr Asn Leu Arg Gly Asn Val Asn Leu Thr Glu Ser Ala Asn Phe Val			
820	825	830	
Leu Gly Lys Ala Asn Leu Phe Gly Thr Ile Gln Ser Arg Gly Asn Ser			
835	840	845	
Gln Val Arg Leu Thr Glu Asn Ser His Trp His Leu Thr Gly Asn Ser			
850	855	860	
Asp Val His Gln Leu Asp Leu Ala Asn Gly His Ile His Leu Asn Ser			
865	870	875	880
Ala Asp Asn Ser Asn Asn Val Thr Lys Tyr Asn Thr Leu Thr Val Asn			
885	890	895	
Ser Leu Ser Gly Asn Gly Ser Phe Tyr Tyr Leu Thr Asp Leu Ser Asn			
900	905	910	
Lys Gln Gly Asp Lys Val Val Val Thr Lys Ser Ala Thr Gly Asn Phe			
915	920	925	
Thr Leu Gln Val Ala Asp Lys Thr Gly Glu Pro Asn His Asn Glu Leu			
930	935	940	
Thr Leu Phe Asp Ala Ser Lys Ala Gln Arg Asp His Leu Asn Val Ser			
945	950	955	960
Leu Val Gly Asn Thr Val Asp Leu Gly Ala Trp Lys Tyr Lys Leu Arg			
965	970	975	
Asn Val Asn Gly Arg Tyr Asp Leu Tyr Asn Pro Glu Val Glu Lys Arg			
980	985	990	
Asn Gln Thr Val Asp Thr Thr Asn Ile Thr Thr Pro Asn Asn Ile Gln			
995	1000	1005	
Ala Asp Val Pro Ser Val Pro Ser Asn Asn Glu Glu Ile Ala Arg Val			
1010	1015	1020	
Asp Glu Ala Pro Val Pro Pro Pro Ala Pro Ala Thr Pro Ser Glu Thr			
1025	1030	1035	1040

Thr Glu Thr Val Ala Glu Asn Ser Lys Gln Glu Ser Lys Thr Val Glu
1045 1050 1055

Lys Asn Glu Gln Asp Ala Thr Glu Thr Thr Ala Gln Asn Arg Glu Val
1060 1065 1070

Ala Lys Glu Ala Lys Ser Asn Val Lys Ala Asn Thr Gln Thr Asn Glu
1075 1080 1085

Val Ala Gln Ser Gly Ser Glu Thr Lys Glu Thr Gln Thr Thr Glu Thr
1090 1095 1100

Lys Glu Thr Ala Thr Val Glu Lys Glu Glu Lys Ala Lys Val Glu Thr
1105 1110 1115 1120

Glu Lys Thr Gln Glu Val Pro Lys Val Thr Ser Gln Val Ser Pro Lys
1125 1130 1135

Gln Glu Gln Ser Glu Thr Val Gln Pro Gln Ala Glu Pro Ala Arg Glu
1140 1145 1150

Asn Asp Pro Thr Val Asn Ile Lys Glu Pro Gln Ser Gln Thr Asn Thr
1155 1160 1165

Thr Ala Asp Thr Glu Gln Pro Ala Lys Glu Thr Ser Ser Asn Val Glu
1170 1175 1180

Gln Pro Val Thr Glu Ser Thr Thr Val Asn Thr Gly Asn Ser Val Val
1185 1190 1195 1200

Glu Asn Pro Glu Asn Thr Thr Pro Ala Thr Thr Gln Pro Thr Val Asn
1205 1210 1215

Ser Glu Ser Ser Asn Lys Pro Lys Asn Arg His Arg Arg Ser Val Arg
1220 1225 1230

Ser Val Pro His Asn Val Glu Pro Ala Thr Thr Ser Ser Asn Asp Arg
1235 1240 1245

Ser Thr Val Ala Leu Cys Asp Leu Thr Ser Thr Asn Thr Asn Ala Val
1250 1255 1260

Leu Ser Asp Ala Arg Ala Lys Ala Gln Phe Val Ala Leu Asn Val Gly
1265 1270 1275 1280

Lys Ala Val Ser Gln His Ile Ser Gln Leu Glu Met Asn Asn Glu Gly
1285 1290 1295

Gln Tyr Asn Val Trp Val Ser Asn Thr Ser Met Asn Lys Asn Tyr Ser
1300 1305 1310

Ser Ser Gln Tyr Arg Arg Phe Ser Ser Lys Ser Thr Gln Thr Gln Leu
1315 1320 1325

Gly Trp Asp Gln Thr Ile Ser Asn Asn Val Gln Leu Gly Gly Val Phe
1330 1335 1340

Thr Tyr Val Arg Asn Ser Asn Asn Phe Asp Lys Ala Thr Ser Lys Asn
1345 1350 1355 1360

Thr Leu Ala Gln Val Asn Phe Tyr Ser Lys Tyr Tyr Ala Asp Asn His
1365 1370 1375

Trp Tyr Leu Gly Ile Asp Leu Gly Tyr Gly Lys Phe Gln Ser Lys Leu
1380 1385 1390

Gln Thr Asn His Asn Ala Lys Phe Ala Arg His Thr Ala Gln Phe Gly

1395	1400	1405
Leu Thr Ala Gly Lys Ala Phe Asn Leu Gly Asn Phe Gly Ile Thr Pro		
1410	1415	1420
Ile Val Gly Val Arg Tyr Ser Tyr Leu Ser Asn Ala Asp Phe Ala Leu		
1425	1430	1435
Asp Gln Ala Arg Ile Lys Val Asn Pro Ile Ser Val Lys Thr Ala Phe		
1445	1450	1455
Ala Gln Val Asp Leu Ser Tyr Thr Tyr His Leu Gly Glu Phe Ser Val		
1460	1465	1470
Thr Pro Ile Leu Ser Ala Arg Tyr Asp Ala Asn Gln Gly Ser Gly Lys		
1475	1480	1485
Ile Asn Val Asn Gly Tyr Asp Phe Ala Tyr Asn Val Glu Asn Gln Gln		
1490	1495	1500
Gln Tyr Asn Ala Gly Leu Lys Leu Lys Tyr His Asn Val Lys Leu Ser		
1505	1510	1515
Leu Ile Gly Gly Leu Thr Lys Ala Lys Gln Ala Glu Lys Gln Lys Thr		
1525	1530	1535
Ala Glu Leu Lys Leu Ser Phe Ser Phe		
1540	1545	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1702 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Leu	Asn	Lys	Lys	Phe	Lys	Leu	Asn	Phe	Ile	Ala	Leu	Thr	Val	Ala		
1															15		
Tyr Ala Leu Thr Pro Tyr Thr Glu Ala Ala Leu Val Arg Asp Asp Val																	
														20	25	30	
Asp Tyr Gln Ile Phe Arg Asp Phe Ala Glu Asn Lys Gly Arg Phe Ser																	
														35	40	45	
Val Gly Ala Thr Asn Val Glu Val Arg Asp Lys Asn Asn His Ser Leu																	
														50	55	60	
Gly Asn Val Leu Pro Asn Gly Ile Pro Met Ile Asp Phe Ser Val Val																	
														65	70	75	80
Asp Val Asp Lys Arg Ile Ala Thr Leu Ile Asn Pro Gln Tyr Val Val																	
														85	90	95	
Gly Val Lys His Val Ser Asn Gly Val Ser Glu Leu His Phe Gly Asn																	
														100	105	110	
Leu Asn Gly Asn Met Asn Asn Gly Asn Asp Lys Ser His Arg Asp Val																	
														115	120	125	
Ser Ser Glu Glu Asn Arg Tyr Phe Ser Val Glu Lys Asn Glu Tyr Pro																	
														130	135	140	
Thr Lys Leu Asn Gly Lys Ala Val Thr Thr Glu Asp Gln Thr Gln Lys																	

145 150 155 160
Arg Arg Glu Asp Tyr Tyr Met Pro Arg Leu Asp Lys Phe Val Thr Glu
165 170 175
Val Ala Pro Ile Glu Ala Ser Thr Ala Ser Ser Asp Ala Gly Thr Tyr
180 185 190
Asn Asp Gln Asn Lys Tyr Pro Ala Phe Val Arg Leu Gly Ser Gly Thr
195 200 205
Gln Phe Ile Tyr Lys Lys Gly Asp Asn Tyr Ser Leu Ile Leu Asn Asn
210 215 220
His Glu Val Gly Gly Asn Asn Leu Lys Leu Val Gly Asp Ala Tyr Thr
225 230 235 240
Tyr Gly Ile Ala Gly Thr Pro Tyr Lys Val Asn His Glu Asn Asn Gly
245 250 255
Leu Ile Gly Phe Gly Asn Ser Lys Glu Glu His Ser Asp Pro Lys Gly
260 265 270
Ile Leu Ser Gln Asp Pro Leu Thr Asn Tyr Ala Val Leu Gly Asp Ser
275 280 285
Gly Ser Pro Leu Phe Val Tyr Asp Arg Glu Lys Gly Lys Trp Leu Phe
290 295 300
Leu Gly Ser Tyr Asp Phe Trp Ala Gly Tyr Asn Lys Lys Ser Trp Gln
305 310 315 320
Glu Trp Asn Ile Tyr Lys Pro Glu Phe Ala Lys Thr Val Leu Asp Lys
325 330 335
Asp Thr Ala Gly Ser Leu Ile Gly Ser Asn Thr Gln Tyr Asn Trp Asn
340 345 350
Pro Thr Gly Lys Thr Ser Val Ile Ser Asn Gly Ser Glu Ser Leu Asn
355 360 365
Val Asp Leu Phe Asp Ser Ser Gln Asp Thr Asp Ser Lys Lys Asn Asn
370 375 380
His Gly Lys Ser Val Thr Leu Arg Gly Ser Gly Thr Leu Thr Leu Asn
385 390 395 400
Asn Asn Ile Asp Gln Gly Ala Gly Gly Leu Phe Phe Glu Gly Asp Tyr
405 410 415
Glu Val Lys Gly Thr Ser Asp Ser Thr Thr Trp Lys Gly Ala Gly Val
420 425 430
Ser Val Ala Asp Gly Lys Thr Val Thr Trp Lys Val His Asn Pro Lys
435 440 445
Ser Asp Arg Leu Ala Lys Ile Gly Lys Gly Thr Leu Ile Val Glu Gly
450 455 460
Lys Gly Glu Asn Lys Gly Ser Leu Lys Val Gly Asp Gly Thr Val Ile
465 470 475 480
Leu Lys Gln Gln Ala Asp Ala Asn Asn Lys Val Lys Ala Phe Ser Gln
485 490 495
Val Gly Ile Val Ser Gly Arg Ser Thr Val Val Leu Asn Asp Asp Lys
500 505 510

Gln Val Asp Pro Asn Ser Ile Tyr Phe Gly Phe Arg Gly Arg Leu
515 520 525

Asp Ala Asn Gly Asn Asn Leu Thr Phe Glu His Ile Arg Asn Ile Asp
530 535 540

Asp Gly Ala Arg Leu Val Asn His Asn Thr Ser Lys Thr Ser Thr Val
545 550 555 560

Thr Ile Thr Gly Glu Ser Leu Ile Thr Asp Pro Asn Thr Ile Thr Pro
565 570 575

Tyr Asn Ile Asp Ala Pro Asp Glu Asp Asn Pro Tyr Ala Phe Arg Arg
580 585 590

Ile Lys Asp Gly Gly Gln Leu Tyr Leu Asn Leu Glu Asn Tyr Thr Tyr
595 600 605

Tyr Ala Leu Arg Lys Gly Ala Ser Thr Arg Ser Glu Leu Pro Lys Asn
610 615 620

Ser Gly Glu Ser Asn Glu Asn Trp Leu Tyr Met Gly Lys Thr Ser Asp
625 630 635 640

Ala Ala Lys Arg Asn Val Met Asn His Ile Asn Asn Glu Arg Met Asn
645 650 655

Gly Phe Asn Gly Tyr Phe Gly Glu Glu Gly Lys Asn Asn Gly Asn
660 665 670

Leu Asn Val Thr Phe Lys Gly Lys Ser Glu Gln Asn Arg Phe Leu Leu
675 680 685

Thr Gly Gly Thr Asn Leu Asn Gly Asp Leu Lys Val Glu Lys Gly Thr
690 695 700

Leu Phe Leu Ser Gly Arg Pro Thr Pro His Ala Arg Asp Ile Ala Gly
705 710 715 720

Ile Ser Ser Thr Lys Lys Asp Gln His Phe Ala Glu Asn Asn Glu Val
725 730 735

Val Val Glu Asp Asp Trp Ile Asn Arg Asn Phe Lys Ala Thr Asn Ile
740 745 750

Asn Val Thr Asn Asn Ala Thr Leu Tyr Ser Gly Arg Asn Val Ala Asn
755 760 765

Ile Thr Ser Asn Ile Thr Ala Ser Asp Asn Ala Lys Val His Ile Gly
770 775 780

Tyr Lys Ala Gly Asp Thr Val Cys Val Arg Ser Asp Tyr Thr Gly Tyr
785 790 795 800

Val Thr Cys Thr Thr Asp Lys Leu Ser Asp Lys Ala Leu Asn Ser Phe
805 810 815

Asn Ala Thr Asn Val Ser Gly Asn Val Asn Leu Ser Gly Asn Ala Asn
820 825 830

Phe Val Leu Gly Lys Ala Asn Leu Phe Gly Thr Ile Ser Gly Thr Gly
835 840 845

Asn Ser Gln Val Arg Leu Thr Glu Asn Ser His Trp His Leu Thr Gly
850 855 860

Asp Ser Asn Val Asn Gln Leu Asn Leu Asp Lys Gly His Ile His Leu

865	870	875	880
Asn Ala Gln Asn Asp Ala Asn Lys Val Thr Thr Tyr Asn Thr Leu Thr			
885	890	895	
Val Asn Ser Leu Ser Gly Asn Gly Ser Phe Tyr Tyr Leu Thr Asp Leu			
900	905	910	
Ser Asn Lys Gln Gly Asp Lys Val Val Val Thr Lys Ser Ala Thr Gly			
915	920	925	
Asn Phe Thr Leu Gln Val Ala Asp Lys Thr Gly Glu Pro Thr Lys Asn			
930	935	940	
Glu Leu Thr Leu Phe Asp Ala Ser Asn Ala Thr Arg Asn Asn Leu Asn			
945	950	955	960
Val Ser Leu Val Gly Asn Thr Val Asp Leu Gly Ala Trp Lys Tyr Lys			
965	970	975	
Leu Arg Asn Val Asn Gly Arg Tyr Asp Leu Tyr Asn Pro Glu Val Glu			
980	985	990	
Lys Arg Asn Gln Thr Val Asp Thr Thr Asn Ile Thr Thr Pro Asn Asn			
995	1000	1005	
Ile Gln Ala Asp Val Pro Ser Val Pro Ser Asn Asn Glu Glu Ile Ala			
1010	1015	1020	
Arg Val Glu Thr Pro Val Pro Pro Ala Pro Ala Thr Pro Ser Glu			
1025	1030	1035	1040
Thr Thr Glu Thr Val Ala Glu Asn Ser Lys Gln Glu Ser Lys Thr Val			
1045	1050	1055	
Glu Lys Asn Glu Gln Asp Ala Thr Glu Thr Thr Ala Gln Asn Gly Glu			
1060	1065	1070	
Val Ala Glu Glu Ala Lys Pro Ser Val Lys Ala Asn Thr Gln Thr Asn			
1075	1080	1085	
Glu Val Ala Gln Ser Gly Ser Glu Thr Glu Glu Thr Gln Thr Thr Glu			
1090	1095	1100	
Ile Lys Glu Thr Ala Lys Val Glu Lys Glu Glu Lys Ala Lys Val Glu			
1105	1110	1115	1120
Lys Glu Glu Lys Ala Lys Val Glu Lys Asp Glu Ile Gln Glu Ala Pro			
1125	1130	1135	
Gln Met Ala Ser Glu Thr Ser Pro Lys Gln Ala Lys Pro Ala Pro Lys			
1140	1145	1150	
Glu Val Ser Thr Asp Thr Lys Val Glu Glu Thr Gln Val Gln Ala Gln			
1155	1160	1165	
Pro Gln Thr Gln Ser Thr Thr Val Ala Ala Ala Glu Ala Thr Ser Pro			
1170	1175	1180	
Asn Ser Lys Pro Ala Glu Glu Thr Gln Pro Ser Glu Lys Thr Asn Ala			
1185	1190	1195	1200
Glu Pro Val Thr Pro Val Val Ser Lys Asn Gln Thr Glu Asn Thr Thr			
1205	1210	1215	
Asp Gln Pro Thr Glu Arg Glu Lys Thr Ala Lys Val Glu Thr Glu Lys			
1220	1225	1230	

Thr Gln Glu Pro Pro Gln Val Ala Ser Gln Ala Ser Pro Lys Gln Glu
1235 1240 1245

Gln Ser Glu Thr Val Gln Pro Gln Ala Val Leu Glu Ser Glu Asn Val
1250 1255 1260

Pro Thr Val Asn Asn Ala Glu Glu Val Gln Ala Gln Leu Gln Thr Gln
1265 1270 1275 1280

Thr Ser Ala Thr Val Ser Thr Lys Gln Pro Ala Pro Glu Asn Ser Ile
1285 1290 1295

Asn Thr Gly Ser Ala Thr Ala Ile Thr Glu Thr Ala Glu Lys Ser Asp
1300 1305 1310

Lys Pro Gln Thr Glu Thr Ala Ala Ser Thr Glu Asp Ala Ser Gln His
1315 1320 1325

Lys Ala Asn Thr Val Ala Asp Asn Ser Val Ala Asn Asn Ser Glu Ser
1330 1335 1340

Ser Glu Pro Lys Ser Arg Arg Arg Arg Ser Ile Ser Gln Pro Gln Glu
1345 1350 1355 1360

Thr Ser Ala Glu Glu Thr Thr Ala Ala Ser Thr Asp Glu Thr Thr Ile
1365 1370 1375

Ala Asp Asn Ser Lys Arg Ser Lys Pro Asn Arg Arg Ser Arg Arg Ser
1380 1385 1390

Val Arg Ser Glu Pro Thr Val Thr Asn Gly Ser Asp Arg Ser Thr Val
1395 1400 1405

Ala Leu Arg Asp Leu Thr Ser Thr Asn Thr Asn Ala Val Ile Ser Asp
1410 1415 1420

Ala Met Ala Lys Ala Gln Phe Val Ala Leu Asn Val Gly Lys Ala Val
1425 1430 1435 1440

Ser Gln His Ile Ser Gln Leu Glu Met Asn Asn Glu Gly Gln Tyr Asn
1445 1450 1455

Val Trp Val Ser Asn Thr Ser Met Asn Glu Asn Tyr Ser Ser Gln
1460 1465 1470

Tyr Arg Arg Phe Ser Ser Lys Ser Thr Gln Thr Gln Leu Gly Trp Asp
1475 1480 1485

Gln Thr Ile Ser Asn Asn Val Gln Leu Gly Gly Val Phe Thr Tyr Val
1490 1495 1500

Arg Asn Ser Asn Asn Phe Asp Lys Ala Ser Ser Lys Asn Thr Leu Ala
1505 1510 1515 1520

Gln Val Asn Phe Tyr Ser Lys Tyr Tyr Ala Asp Asn His Trp Tyr Leu
1525 1530 1535

Gly Ile Asp Leu Gly Tyr Gly Lys Phe Gln Ser Asn Leu Lys Thr Asn
1540 1545 1550

His Asn Ala Lys Phe Ala Arg His Thr Ala Gln Phe Gly Leu Thr Ala
1555 1560 1565

Gly Lys Ala Phe Asn Leu Gly Asn Phe Gly Ile Thr Pro Ile Val Gly
1570 1575 1580

Val Arg Tyr Ser Tyr Leu Ser Asn Ala Asn Phe Ala Leu Ala Lys Asp

1585	1590	1595	1600
Arg Ile Lys Val Asn Pro Ile Ser Val Lys Thr Ala Phe Ala Gln Val			
1605		1610	1615
Asp Leu Ser Tyr Thr Tyr His Leu Gly Glu Phe Ser Val Thr Pro Ile			
1620		1625	1630
Leu Ser Ala Arg Tyr Asp Thr Asn Gln Gly Ser Gly Lys Ile Asn Val			
1635		1640	1645
Asn Gln Tyr Asp Phe Ala Tyr Asn Val Glu Asn Gln Gln Gln Tyr Asn			
1650		1655	1660
Ala Gly Leu Lys Leu Lys Tyr His Asn Val Lys Leu Ser Leu Ile Gly			
1665		1670	1675
Gly Leu Thr Lys Ala Lys Gln Ala Glu Lys Gln Lys Thr Ala Glu Leu			
1685		1690	1695
Lys Leu Ser Phe Ser Phe			
1700			

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1848 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Leu	Asn	Lys	Lys	Phe	Lys	Leu	Asn	Phe	Ile	Ala	Leu	Thr	Val	Ala
1															
Tyr	Ala	Leu	Thr	Pro	Tyr	Thr	Glu	Ala	Ala	Leu	Val	Arg	Asp	Asp	Val
Asp	Tyr	Gln	Ile	Phe	Arg	Asp	Phe	Ala	Glu	Asn	Lys	Gly	Lys	Phe	Ser
Val	Gly	Ala	Thr	Asn	Val	Glu	Val	Arg	Asp	Lys	Lys	Asn	Gln	Ser	Leu
Gly	Ser	Ala	Leu	Pro	Asn	Gly	Ile	Pro	Met	Ile	Asp	Phe	Ser	Val	Val
Asp	Val	Asp	Lys	Arg	Ile	Ala	Thr	Leu	Val	Asn	Pro	Gln	Tyr	Val	Val
Gly	Val	Lys	His	Val	Ser	Asn	Gly	Val	Ser	Glu	Leu	His	Phe	Gly	Asn
Leu	Asn	Gly	Asn	Met	Asn	Asn	Gly	Asn	Ala	Lys	Ser	His	Arg	Asp	Val
Ser	Ser	Glu	Glu	Asn	Arg	Tyr	Tyr	Thr	Val	Glu	Lys	Asn	Asn	Phe	Pro
Thr	Glu	Asn	Val	Thr	Ser	Phe	Thr	Lys	Glu	Glu	Gln	Asp	Ala	Gln	Lys
Arg	Arg	Glu	Asp	Tyr	Tyr	Met	Pro	Arg	Leu	Asp	Lys	Phe	Val	Thr	Glu
Val	Ala	Pro	Ile	Glu	Ala	Ser	Thr	Ala	Asn	Asn	Lys	Gly	Glu	Tyr	

180	185	190
Asn Asn Ser Asp Lys Tyr Pro Ala Phe Val Arg Leu Gly Ser Gly Thr		
195	200	205
Gln Phe Ile Tyr Lys Lys Gly Ser Arg Tyr Gln Leu Ile Leu Thr Glu		
210	215	220
Lys Asp Lys Gln Gly Asn Leu Leu Arg Asn Trp Asp Val Gly Gly Asp		
225	230	235
Asn Leu Glu Leu Val Gly Asn Ala Tyr Thr Tyr Gly Ile Ala Gly Thr		
245	250	255
Pro Tyr Lys Val Asn His Glu Asn Asn Gly Leu Ile Gly Phe Gly Asn		
260	265	270
Ser Lys Glu Glu His Ser Asp Pro Lys Gly Ile Leu Ser Gln Asp Pro		
275	280	285
Leu Thr Asn Tyr Ala Val Leu Gly Asp Ser Gly Ser Pro Leu Phe Val		
290	295	300
Tyr Asp Arg Glu Lys Gly Lys Trp Leu Phe Leu Gly Ser Tyr Asp Phe		
305	310	315
Trp Ala Gly Tyr Asn Lys Ser Trp Gln Glu Trp Asn Ile Tyr Lys		
325	330	335
His Glu Phe Ala Glu Lys Ile Tyr Gln Gln Tyr Ser Ala Gly Ser Leu		
340	345	350
Ile Gly Ser Asn Thr Gln Tyr Thr Trp Gln Ala Thr Gly Ser Thr Ser		
355	360	365
Thr Ile Thr Gly Gly Glu Pro Leu Ser Val Asp Leu Thr Asp Gly		
370	375	380
Lys Asp Lys Pro Asn His Gly Lys Ser Ile Thr Leu Lys Gly Ser Gly		
385	390	395
Thr Leu Thr Leu Asn Asn His Ile Asp Gln Gly Ala Gly Gly Leu Phe		
405	410	415
Phe Glu Gly Asp Tyr Glu Val Lys Gly Thr Ser Asp Ser Thr Thr Trp		
420	425	430
Lys Gly Ala Gly Val Ser Val Ala Asp Gly Lys Thr Val Thr Trp Lys		
435	440	445
Val His Asn Pro Lys Tyr Asp Arg Leu Ala Lys Ile Gly Lys Gly Thr		
450	455	460
Leu Val Val Glu Gly Lys Gly Lys Asn Glu Gly Leu Leu Lys Val Gly		
465	470	475
Asp Gly Thr Val Ile Leu Lys Gln Lys Ala Asp Ala Asn Asn Lys Val		
485	490	495
Gln Ala Phe Ser Gln Val Gly Ile Val Ser Gly Arg Ser Thr Leu Val		
500	505	510
Leu Asn Asp Asp Lys Gln Val Asp Pro Asn Ser Ile Tyr Phe Gly Phe		
515	520	525
Arg Gly Gly Arg Leu Asp Leu Asn Gly Asn Ser Leu Thr Phe Asp His		
530	535	540

Ile Arg Asn Ile Asp Asp Gly Ala Arg Val Val Asn His Asn Met Thr
545 550 555 560
Asn Thr Ser Asn Ile Thr Ile Thr Gly Glu Ser Leu Ile Thr Asn Pro
565 570 575
Asn Thr Ile Thr Ser Tyr Asn Ile Glu Ala Gln Asp Asp Asp His Pro
580 585 590 595
Leu Arg Ile Arg Ser Ile Pro Tyr Arg Gln Leu Tyr Phe Asn Gln Asp
595 600 605
Asn Arg Ser Tyr Tyr Thr Leu Lys Lys Gly Ala Ser Thr Arg Ser Glu
610 615 620
Leu Pro Gln Asn Ser Gly Glu Ser Asn Glu Asn Trp Leu Tyr Met Gly
625 630 635 640
Arg Thr Ser Asp Ala Ala Lys Arg Asn Val Met Asn His Ile Asn Asn
645 650 655
Glu Arg Met Asn Gly Phe Asn Gly Tyr Phe Gly Glu Glu Thr Lys
660 665 670
Ala Thr Gln Asn Gly Lys Leu Asn Val Thr Phe Asn Gly Lys Ser Asp
675 680 685
Gln Asn Arg Phe Leu Leu Thr Gly Gly Thr Asn Leu Asn Gly Asp Leu
690 695 700
Asn Val Glu Lys Gly Thr Leu Phe Leu Ser Gly Arg Pro Thr Pro His
705 710 715 720
Ala Arg Asp Ile Ala Gly Ile Ser Ser Thr Lys Lys Asp Pro His Phe
725 730 735
Thr Glu Asn Asn Glu Val Val Glu Asp Asp Trp Ile Asn Arg Asn
740 745 750
Phe Lys Ala Thr Thr Met Asn Val Thr Gly Asn Ala Ser Leu Tyr Ser
755 760 765
Gly Arg Asn Val Ala Asn Ile Thr Ser Asn Ile Thr Ala Ser Asn Asn
770 775 780
Ala Gln Val His Ile Gly Tyr Lys Thr Gly Asp Thr Val Cys Val Arg
785 790 795 800
Ser Asp Tyr Thr Gly Tyr Val Thr Cys His Asn Ser Asn Leu Ser Glu
805 810 815
Lys Ala Leu Asn Ser Phe Asn Pro Thr Asn Leu Arg Gly Asn Val Asn
820 825 830
Leu Thr Glu Asn Ala Ser Phe Thr Leu Gly Lys Ala Asn Leu Phe Gly
835 840 845
Thr Ile Gln Ser Ile Gly Thr Ser Gln Val Asn Leu Lys Glu Asn Ser
850 855 860
His Trp His Leu Thr Gly Asn Ser Asn Val Asn Gln Leu Asn Leu Thr
865 870 875 880
Asn Gly His Ile His Leu Asn Ala Gln Asn Asp Ala Asn Lys Val Thr
885 890 895
Thr Tyr Asn Thr Leu Thr Val Asn Ser Leu Ser Gly Asn Gly Ser Phe

900	905	910
Tyr Tyr Trp Val Asp Phe Thr Asn Asn Lys Ser Asn Lys Val Val Val		
915	920	925
Asn Lys Ser Ala Thr Gly Asn Phe Thr Leu Gln Val Ala Asp Lys Thr		
930	935	940
Gly Glu Pro Asn His Asn Glu Leu Thr Leu Phe Asp Ala Ser Asn Ala		
945	950	955
Thr Arg Asn Asn Leu Glu Val Thr Leu Ala Asn Gly Ser Val Asp Arg		
965	970	975
Gly Ala Trp Lys Tyr Lys Leu Arg Asn Val Asn Gly Arg Tyr Asp Leu		
980	985	990
Tyr Asn Pro Glu Val Glu Lys Arg Asn Gln Thr Val Asp Thr Thr Asn		
995	1000	1005
Ile Thr Thr Pro Asn Asp Ile Gln Ala Asp Ala Pro Ser Ala Gln Ser		
1010	1015	1020
Asn Asn Glu Glu Ile Ala Arg Val Glu Thr Pro Val Pro Pro Pro Ala		
1025	1030	1035
Pro Ala Thr Glu Ser Ala Ile Ala Ser Glu Gln Pro Glu Thr Arg Pro		
1045	1050	1055
Ala Glu Thr Ala Gln Pro Ala Met Glu Glu Thr Asn Thr Ala Asn Ser		
1060	1065	1070
Thr Glu Thr Ala Pro Lys Ser Asp Thr Ala Thr Gln Thr Glu Asn Pro		
1075	1080	1085
Asn Ser Glu Ser Val Pro Ser Glu Thr Thr Glu Lys Val Ala Glu Asn		
1090	1095	1100
Pro Pro Gln Glu Asn Glu Thr Val Ala Lys Asn Glu Gln Glu Ala Thr		
1105	1110	1115
Glu Pro Thr Pro Gln Asn Gly Glu Val Ala Lys Glu Asp Gln Pro Thr		
1125	1130	1135
Val Glu Ala Asn Thr Gln Thr Asn Glu Ala Thr Gln Ser Glu Gly Lys		
1140	1145	1150
Thr Glu Glu Thr Gln Thr Ala Glu Thr Lys Ser Glu Pro Thr Glu Ser		
1155	1160	1165
Val Thr Val Ser Glu Asn Gln Pro Glu Lys Thr Val Ser Gln Ser Thr		
1170	1175	1180
Glu Asp Lys Val Val Val Glu Lys Glu Glu Lys Ala Lys Val Glu Thr		
1185	1190	1195
Glu Glu Thr Gln Lys Ala Pro Gln Val Thr Ser Lys Glu Pro Pro Lys		
1205	1210	1215
Gln Ala Glu Pro Ala Pro Glu Glu Val Pro Thr Asp Thr Asn Ala Glu		
1220	1225	1230
Glu Ala Gln Ala Leu Gln Gln Thr Gln Pro Thr Thr Val Ala Ala Ala		
1235	1240	1245
Glu Thr Thr Ser Pro Asn Ser Lys Pro Ala Glu Glu Thr Gln Gln Pro		
1250	1255	1260

Ser Glu Lys Thr Asn Ala Glu Pro Val Thr Pro Val Val Ser Glu Asn
1265 1270 1275 1280

Thr Ala Thr Gln Pro Thr Glu Thr Glu Glu Thr Ala Lys Val Glu Lys
1285 1290 1295

Glu Lys Thr Gln Glu Val Pro Gln Val Ala Ser Gln Glu Ser Pro Lys
1300 1305 1310

Gln Glu Gln Pro Ala Ala Lys Pro Gln Ala Gln Thr Lys Pro Gln Ala
1315 1320 1325

Glu Pro Ala Arg Glu Asn Val Leu Thr Thr Lys Asn Val Gly Glu Pro
1330 1335 1340

Gln Pro Gln Ala Gln Pro Gln Thr Gln Ser Thr Ala Val Pro Thr Thr
1345 1350 1355 1360

Gly Glu Thr Ala Ala Asn Ser Lys Pro Ala Ala Lys Pro Gln Ala Gln
1365 1370 1375

Ala Lys Pro Gln Thr Glu Pro Ala Arg Glu Asn Val Ser Thr Val Asn
1380 1385 1390

Thr Lys Glu Pro Gln Ser Gln Thr Ser Ala Thr Val Ser Thr Glu Gln
1395 1400 1405

Pro Ala Lys Glu Thr Ser Ser Asn Val Glu Gln Pro Ala Pro Glu Asn
1410 1415 1420

Ser Ile Asn Thr Gly Ser Ala Thr Thr Met Thr Glu Thr Ala Glu Lys
1425 1430 1435 1440

Ser Asp Lys Pro Gln Met Glu Thr Val Thr Glu Asn Asp Arg Gln Pro
1445 1450 1455

Glu Ala Asn Thr Val Ala Asp Asn Ser Val Ala Asn Asn Ser Glu Ser
1460 1465 1470

Ser Glu Ser Lys Ser Arg Arg Arg Arg Ser Val Ser Gln Pro Lys Glu
1475 1480 1485

Thr Ser Ala Glu Glu Thr Thr Val Ala Ser Thr Gln Glu Thr Thr Val
1490 1495 1500

Asp Asn Ser Val Ser Thr Pro Lys Pro Arg Ser Arg Arg Thr Arg Arg
1505 1510 1515 1520

Ser Val Gln Thr Asn Ser Tyr Glu Pro Val Glu Leu Pro Thr Glu Asn
1525 1530 1535

Ala Glu Asn Ala Glu Asn Val Gln Ser Gly Asn Asn Val Ala Asn Ser
1540 1545 1550

Gln Pro Ala Leu Arg Asn Leu Thr Ser Lys Asn Thr Asn Ala Val Ile
1555 1560 1565

Ser Asn Ala Met Ala Lys Ala Gln Phe Val Ala Leu Asn Val Gly Lys
1570 1575 1580

Ala Val Ser Gln His Ile Ser Gln Leu Glu Met Asn Asn Glu Gly Gln
1585 1590 1595 1600

Tyr Asn Val Trp Ile Ser Asn Thr Ser Met Asn Lys Asn Tyr Ser Ser
1605 1610 1615

Glu Gln Tyr Arg Arg Phe Ser Ser Lys Ser Thr Gln Thr Gln Leu Gly

1620	1625	1630
Trp Asp Gln Thr Ile Ser Asn Asn Val Gln Leu Gly Gly Val Phe Thr		
1635	1640	1645
Tyr Val Arg Asn Ser Asn Asn Phe Asp Lys Ala Ser Ser Lys Asn Thr		
1650	1655	1660
Leu Ala Gln Val Asn Phe Tyr Ser Lys Tyr Tyr Ala Asp Asn His Trp		
1665	1670	1675
1680		
Tyr Leu Gly Ile Asp Leu Gly Tyr Gly Lys Phe Gln Ser Asn Leu Gln		
1685	1690	1695
Thr Asn Asn Asn Ala Lys Phe Ala Arg His Thr Ala Gln Ile Gly Leu		
1700	1705	1710
Thr Ala Gly Lys Ala Phe Asn Leu Gly Asn Phe Ala Val Lys Pro Thr		
1715	1720	1725
Val Gly Val Arg Tyr Ser Tyr Leu Ser Asn Ala Asp Phe Ala Leu Ala		
1730	1735	1740
Gln Asp Arg Ile Lys Val Asn Pro Ile Ser Val Lys Thr Ala Phe Ala		
1745	1750	1755
1760		
Gln Val Asp Leu Ser Tyr Thr Tyr His Leu Gly Glu Phe Ser Ile Thr		
1765	1770	1775
Pro Ile Leu Ser Ala Arg Tyr Asp Ala Asn Gln Gly Asn Gly Lys Ile		
1780	1785	1790
Asn Val Ser Val Tyr Asp Phe Ala Tyr Asn Val Glu Asn Gln Gln Gln		
1795	1800	1805
Tyr Asn Ala Gly Leu Lys Leu Lys Tyr His Asn Val Lys Leu Ser Leu		
1810	1815	1820
Ile Gly Gly Leu Thr Lys Ala Lys Gln Ala Glu Lys Gln Lys Thr Ala		
1825	1830	1835
1840		
Glu Val Lys Leu Ser Phe Ser Phe		
1845		

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Asp Ser Gly Ser Pro Met Phe
 1 5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Asp Ser Gly Ser Pro Leu Phe
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

His Thr Tyr Phe Gly Ile Asp
1 5